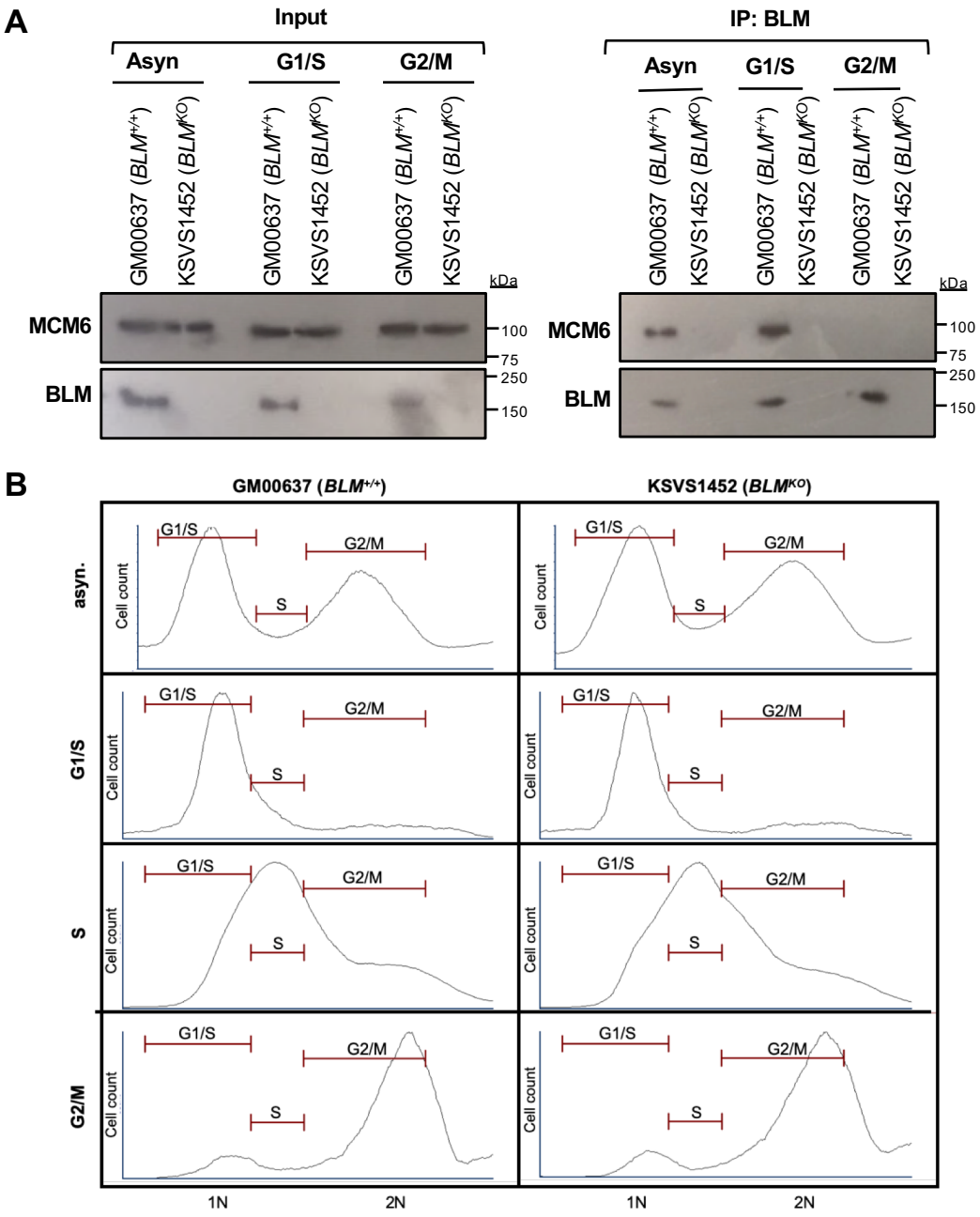
Figure S1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Input
Asyn
G1/S
G2/M
GM00637 (BLM+/+)
KSVS1452 (BLMKO)
kDa
MCM6
BLM
100
75
250
150
IP: BLM
B
GM00637 (BLM+/+)
KSVS1452 (BLMKO)
asyn.
G1/S
S
G2/M
Cell count
1N
2N

Figure S2

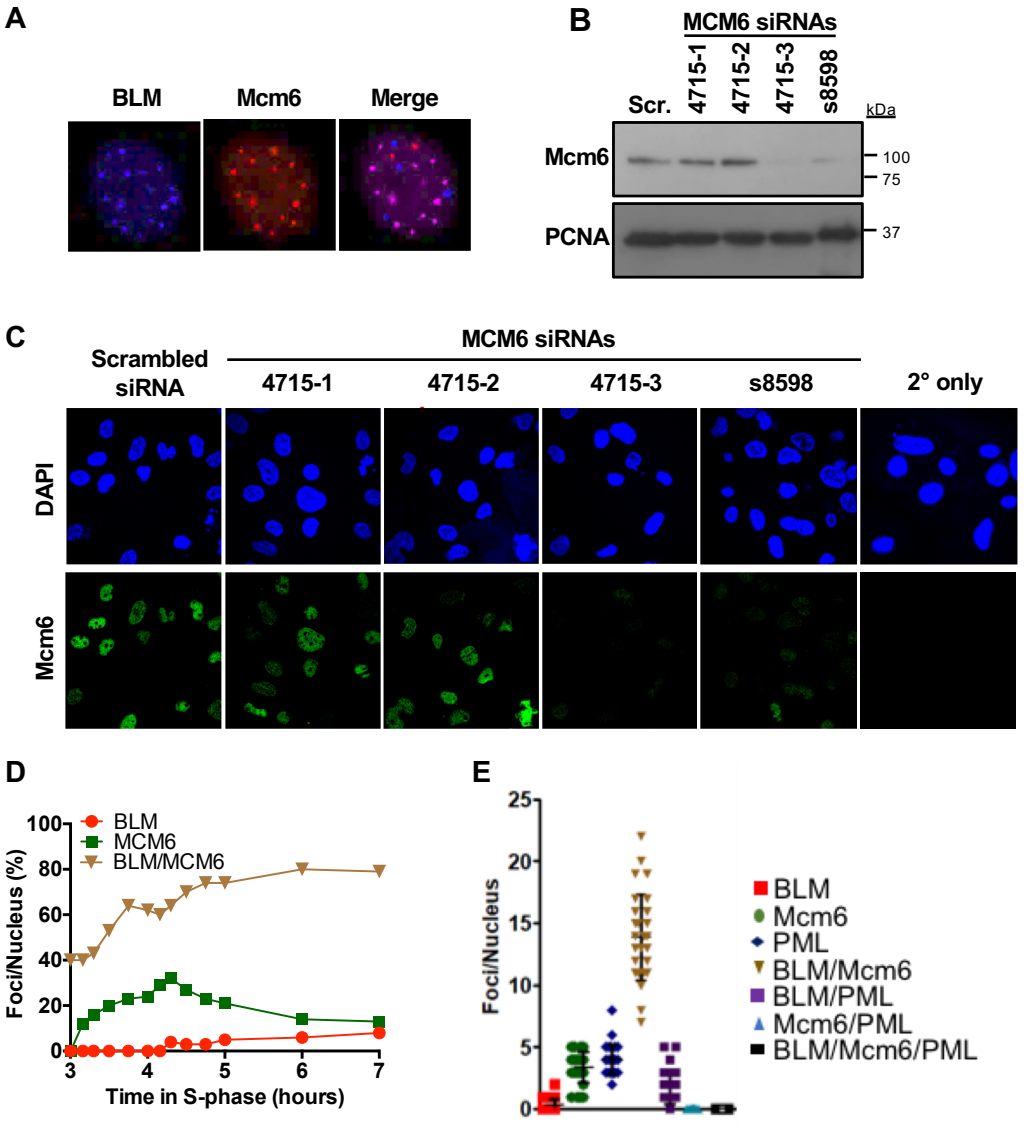
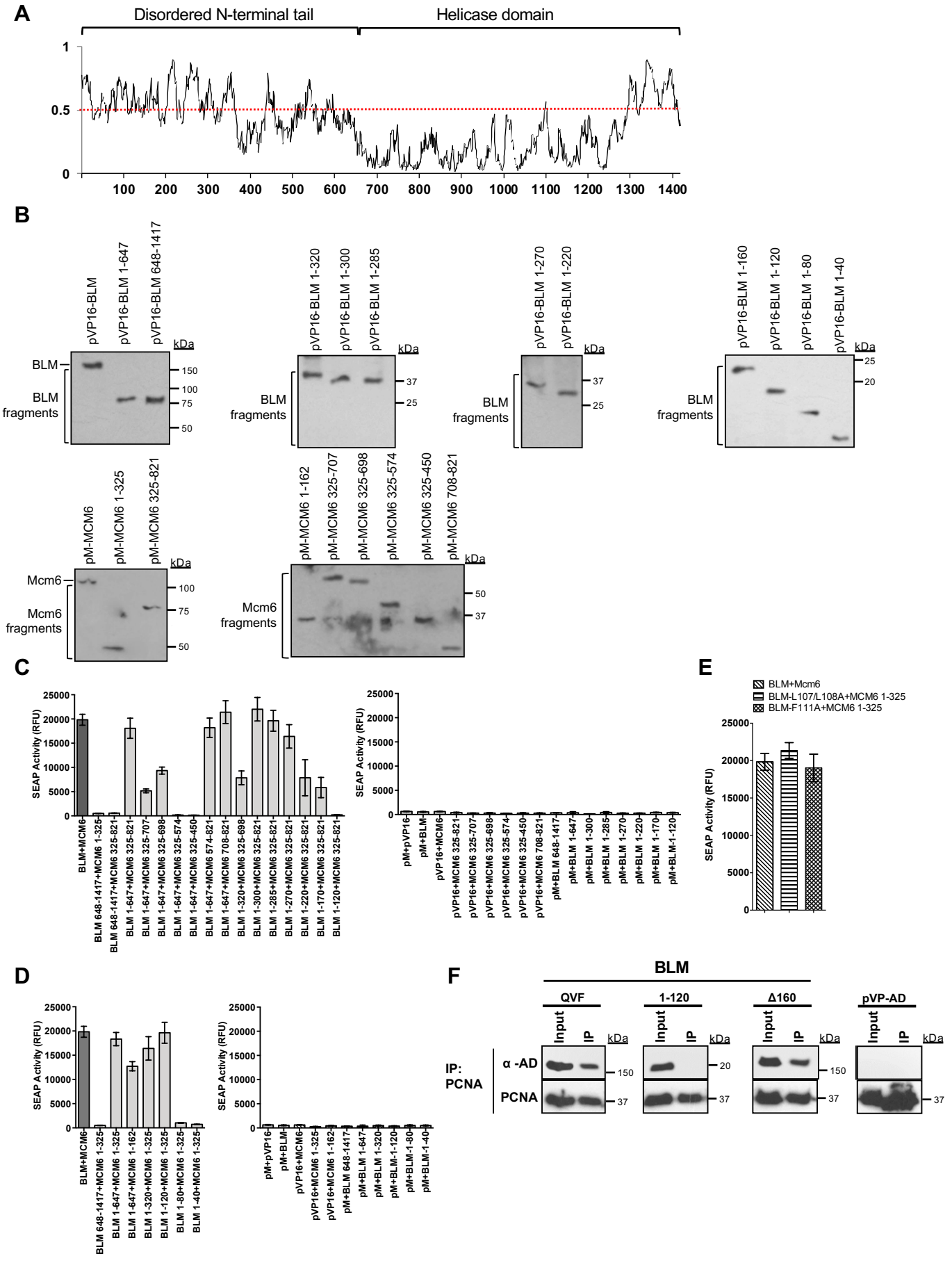

A
BLM
Mcm6
Merge
B
MCM6 siRNAs
Scr.
4715-1
4715-2
4715-3
s8598
kDa
Mcm6
PCNA
100
75
37
C
Scrambled siRNA
MCM6 siRNAs
4715-1
4715-2
4715-3
s8598
2° only
DAPI
Mcm6
D
BLM
MCM6
BLM/MCM6
Foci/Nucleus (%)
Time in S-phase (hours)
E
Foci/Nucleus
BLM
Mcm6
PML
BLM/Mcm6
BLM/PML
Mcm6/PML
BLM/Mcm6/PML

Figure S3


A
Disordered N-terminal tail
Helicase domain
B
pVP16-BLM
pVP16-BLM 1-647
pVP16-BLM 648-1417
pVP16-BLM 1-320
pVP16-BLM 1-300
pVP16-BLM 1-285
pVP16-BLM 1-270
pVP16-BLM 1-220
pVP16-BLM 1-160
pVP16-BLM 1-120
pVP16-BLM 1-80
pVP16-BLM 1-40
pM-MCM6
pM-MCM6 1-325
pM-MCM6 325-821
pM-MCM6 1-162
pM-MCM6 325-707
pM-MCM6 325-698
pM-MCM6 325-574
pM-MCM6 325-450
pM-MCM6 708-821
kDa
BLM
BLM fragments
Mcm6
Mcm6 fragments
C
SEAP Activity (RFU)
BLM+MCM6
BLM 648-1417+MCM6 1-325
BLM 648-1417+MCM6 325-821
BLM 1-647+MCM6 325-821
BLM 1-647+MCM6 325-707
BLM 1-647+MCM6 325-698
BLM 1-647+MCM6 325-574
BLM 1-647+MCM6 325-450
BLM 1-647+MCM6 574-821
BLM 1-647+MCM6 708-821
BLM 1-320+MCM6 325-698
BLM 1-300+MCM6 325-821
BLM 1-285+MCM6 325-821
BLM 1-270+MCM6 325-821
BLM 1-220+MCM6 325-821
BLM 1-170+MCM6 325-821
BLM 1-120+MCM6 325-821
pM+pVP16
pM+BLM
pVP16+MCM6
pVP16+MCM6 325-821
pVP16+MCM6 325-707
pVP16+MCM6 325-698
pVP16+MCM6 325-574
pVP16+MCM6 325-450
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pM+BLM 648-1417
pM+BLM 1-647
pM+BLM 1-300
pM+BLM 1-285
pM+BLM 1-270
pM+BLM 1-220
pM+BLM 1-170
pM+BLM-1-120
D
BLM+MCM6
BLM 648-1417+MCM6 1-325
BLM 1-647+MCM6 1-325
BLM 1-647+MCM6 1-162
BLM 1-320+MCM6 1-325
BLM 1-120+MCM6 1-325
BLM 1-80+MCM6 1-325
BLM 1-40+MCM6 1-325
pM+pVP16
pM+BLM
pVP16+MCM6
pVP16+MCM6 1-325
pVP16+MCM6 1-162
pM+BLM 648-1417
pM+BLM 1-647
pM+BLM 1-320
pM+BLM-1-120
pM+BLM-1-80
pM+BLM-1-40
E
BLM+Mcm6
BLM-L107/L108A+MCM6 1-325
BLM-F111A+MCM6 1-325
SEAP Activity (RFU)
F
BLM
QVF
1-120
Δ160
pVP-AD
Input
IP
kDa
IP: PCNA
α -AD
PCNA

Figure S4

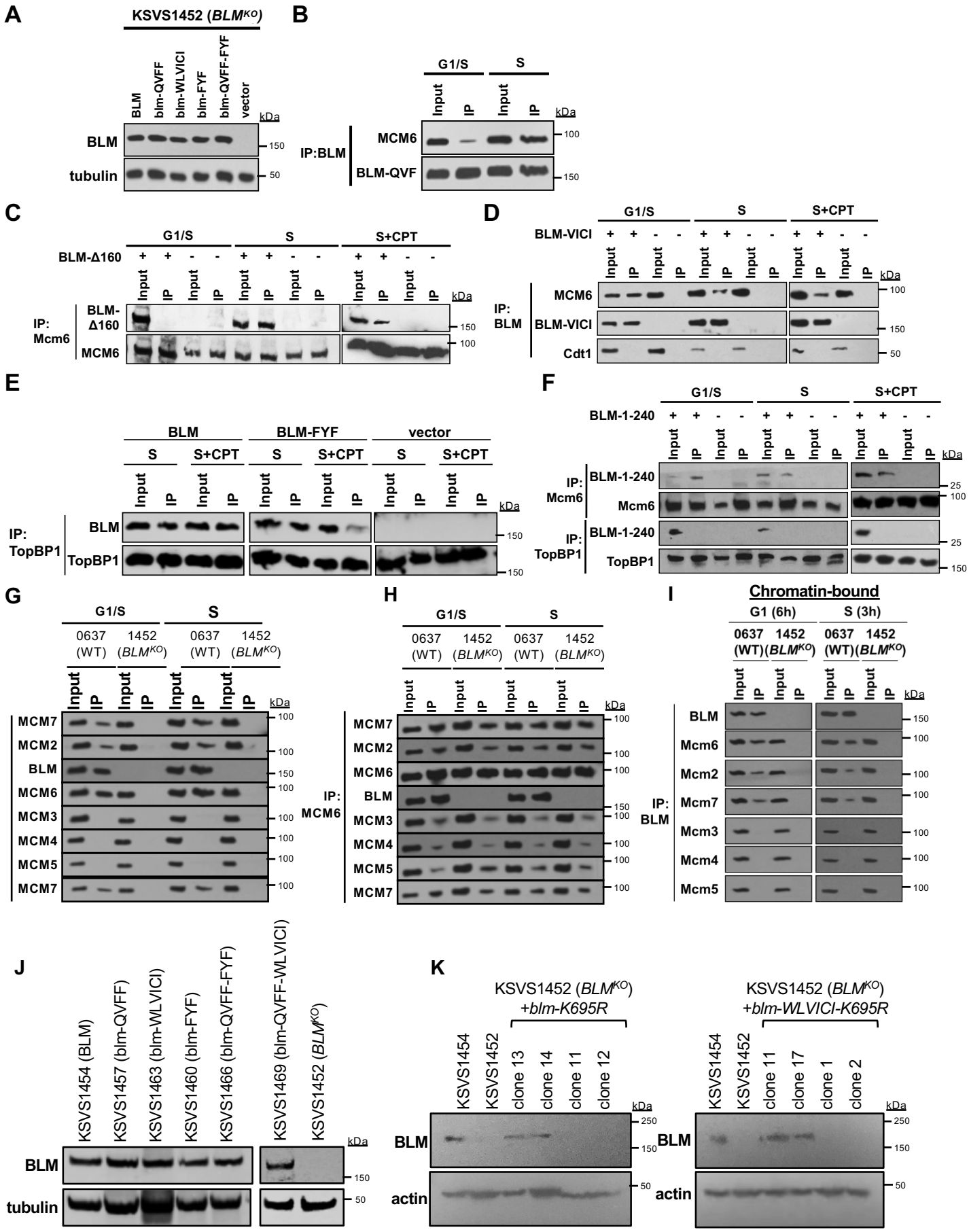

A
KSVS1452 (BLM^KO)
BLM
blm-QVFF
blm-WLVICI
blm-FYF
blm-QVFF-FYF
vector
kDa
BLM
tubulin
150
50
B
G1/S
S
Input
IP
Input
IP
kDa
IP:BLM
MCM6
BLM-QVF
100
150
C
G1/S
S
S+CPT
BLM-Δ160
+ + - - + + - - + + - -
Input IP Input IP Input IP Input IP Input IP Input IP
kDa
IP: Mcm6
BLM-Δ160
MCM6
150
100
D
G1/S
S
S+CPT
BLM-VICI
+ + - - + + - - + + - -
Input IP Input IP Input IP Input IP Input IP Input IP
kDa
IP: BLM
MCM6
BLM-VICI
Cdt1
100
150
50
E
BLM
BLM-FYF
vector
S
S+CPT
S
S+CPT
S
S+CPT
Input IP Input IP Input IP Input IP Input IP Input IP
kDa
IP: TopBP1
BLM
TopBP1
150
150
F
G1/S
S
S+CPT
BLM-1-240
+ + - - + + - - + + - -
Input IP Input IP Input IP Input IP Input IP Input IP
kDa
IP: Mcm6
BLM-1-240
Mcm6
IP: TopBP1
BLM-1-240
TopBP1
25
100
25
150
G
G1/S
S
0637 (WT)
1452 (BLM^KO)
0637 (WT)
1452 (BLM^KO)
Input IP Input IP Input IP Input IP
kDa
IP: BLM
MCM7
MCM2
BLM
MCM6
MCM3
MCM4
MCM5
MCM7
100
100
150
100
100
100
100
100
H
G1/S
S
0637 (WT)
1452 (BLM^KO)
0637 (WT)
1452 (BLM^KO)
Input IP Input IP Input IP Input IP
kDa
IP: MCM6
MCM7
MCM2
MCM6
BLM
MCM3
MCM4
MCM5
MCM7
100
100
100
150
100
100
100
100
I
Chromatin-bound
G1 (6h)
S (3h)
0637 (WT)
1452 (BLM^KO)
0637 (WT)
1452 (BLM^KO)
Input IP Input IP Input IP Input IP
kDa
IP: BLM
BLM
Mcm6
Mcm2
Mcm7
Mcm3
Mcm4
Mcm5
150
100
100
100
100
100
100
J
KSVS1454 (BLM)
KSVS1457 (blm-QVFF)
KSVS1463 (blm-WLVICI)
KSVS1460 (blm-FYF)
KSVS1466 (blm-QVFF-FYF)
KSVS1469 (blm-QVFF-WLVICI)
KSVS1452 (BLM^KO)
kDa
BLM
tubulin
150
50
K
KSVS1452 (BLM^KO) +blm-K695R
KSVS1454
KSVS1452
clone 13
clone 14
clone 11
clone 12
kDa
BLM
actin
250
150
50
KSVS1452 (BLM^KO) +blm-WLVICI-K695R
KSVS1454
KSVS1452
clone 11
clone 17
clone 1
clone 2
kDa
BLM
actin
250
150
50

Figure S5

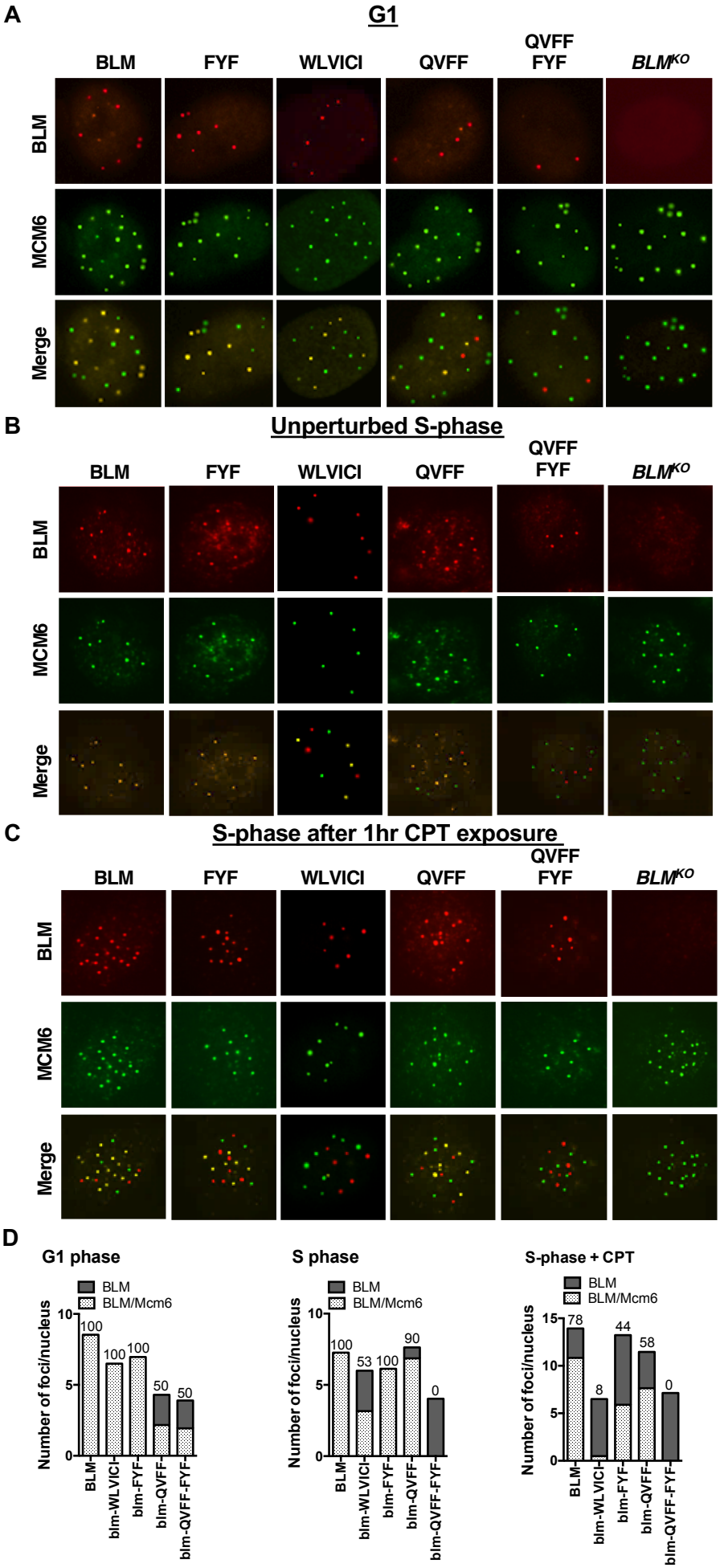

A
G1
BLM
FYF
WLVICI
QVFF
QVFF FYF
BLM^KO
BLM
MCM6
Merge
B
Unperturbed S-phase
C
S-phase after 1hr CPT exposure
D
G1 phase
S phase
S-phase + CPT
BLM
BLM/Mcm6
Number of foci/nucleus
100
100
100
50
50
100
53
100
90
0
78
8
44
58
0
blm-WLVICI
blm-FYF
blm-QVFF
blm-QVFF-FYF

Figure S6

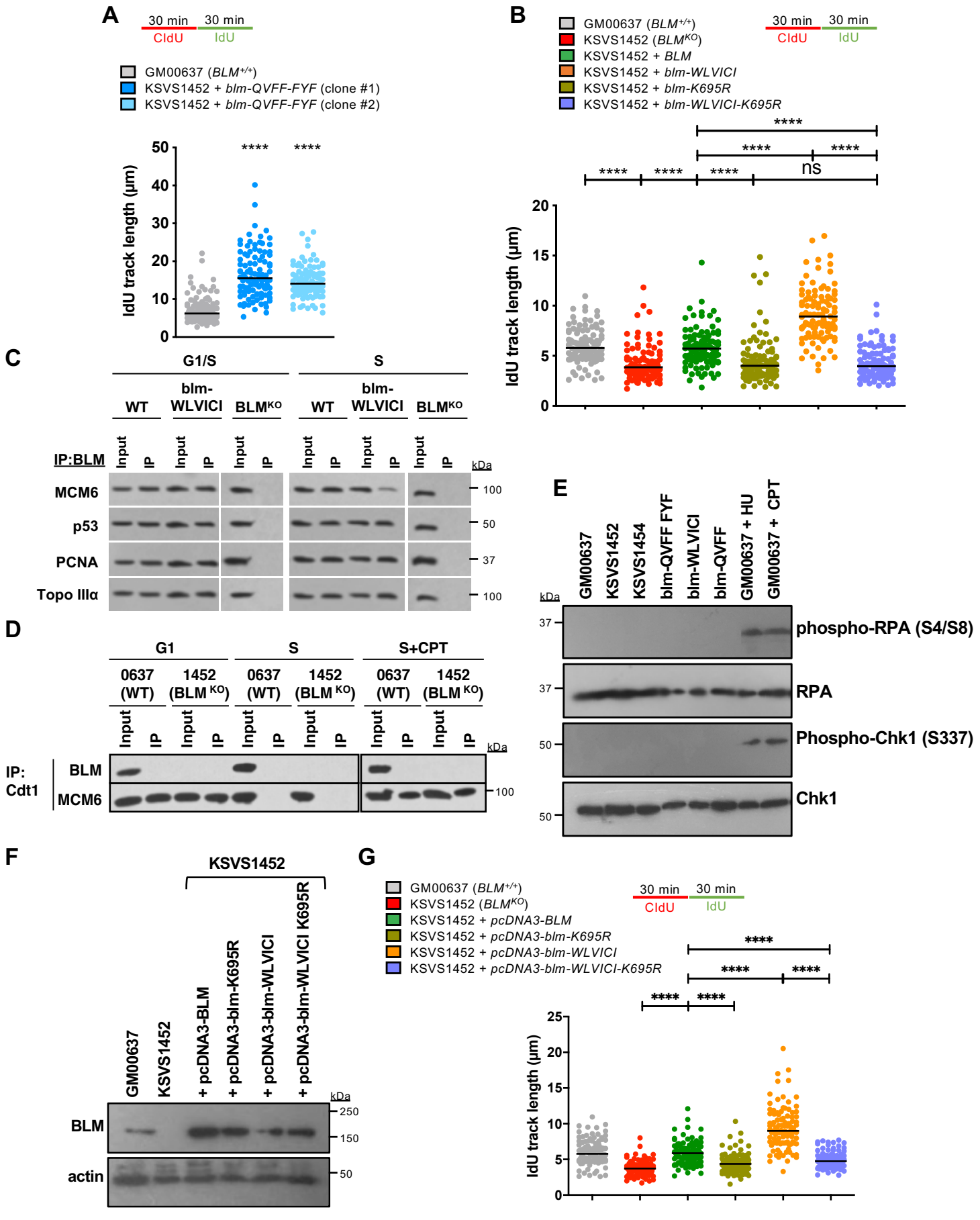
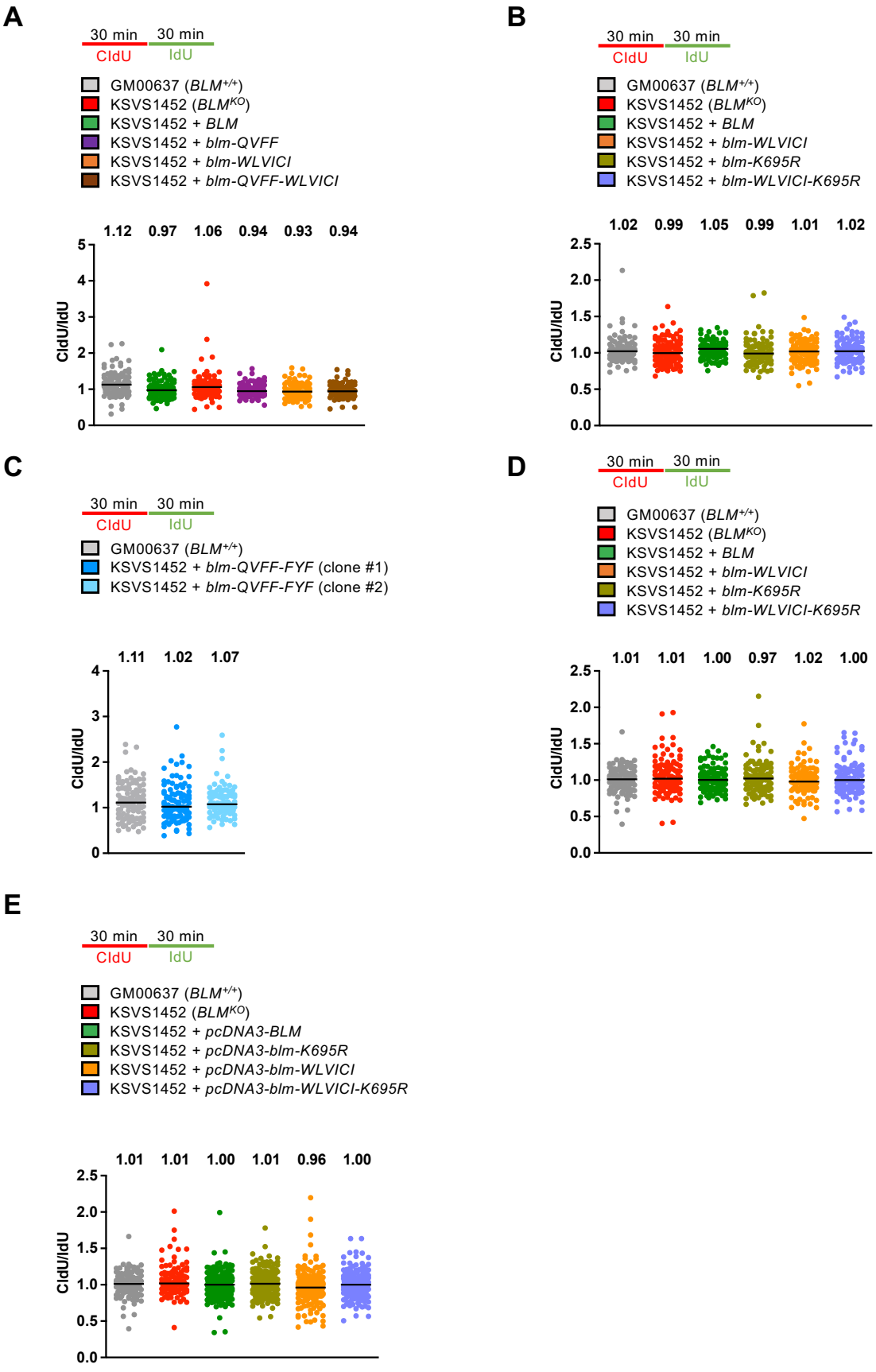

A
30 min CldU
30 min IdU
GM00637 (BLM+/+)
KSVS1452 + blm-QVFF-FYF (clone #1)
KSVS1452 + blm-QVFF-FYF (clone #2)
IdU track length (µm)
****
B
GM00637 (BLM+/+)
KSVS1452 (BLMKO)
KSVS1452 + BLM
KSVS1452 + blm-WLVICI
KSVS1452 + blm-K695R
KSVS1452 + blm-WLVICI-K695R
ns
C
G1/S
S
WT
blm-WLVICI
BLMKO
IP:BLM
Input
IP
kDa
MCM6
p53
PCNA
Topo IIIα
D
G1
S
S+CPT
0637 (WT)
1452 (BLM KO)
IP: Cdt1
BLM
MCM6
E
GM00637
KSVS1452
KSVS1454
blm-QVFF FYF
blm-WLVICI
blm-QVFF
GM00637 + HU
GM00637 + CPT
phospho-RPA (S4/S8)
RPA
Phospho-Chk1 (S337)
Chk1
F
KSVS1452
GM00637
KSVS1452
+ pcDNA3-BLM
+ pcDNA3-blm-K695R
+ pcDNA3-blm-WLVICI
+ pcDNA3-blm-WLVICI K695R
BLM
actin
G
GM00637 (BLM+/+)
KSVS1452 (BLMKO)
KSVS1452 + pcDNA3-BLM
KSVS1452 + pcDNA3-blm-K695R
KSVS1452 + pcDNA3-blm-WLVICI
KSVS1452 + pcDNA3-blm-WLVICI-K695R
IdU track length (µm)

Figure S7


A
30 min
CldU
30 min
IdU
GM00637 (BLM+/+)
KSVS1452 (BLMKO)
KSVS1452 + BLM
KSVS1452 + blm-QVFF
KSVS1452 + blm-WLVICI
KSVS1452 + blm-QVFF-WLVICI
1.12 0.97 1.06 0.94 0.93 0.94
CldU/IdU
B
30 min
CldU
30 min
IdU
GM00637 (BLM+/+)
KSVS1452 (BLMKO)
KSVS1452 + BLM
KSVS1452 + blm-WLVICI
KSVS1452 + blm-K695R
KSVS1452 + blm-WLVICI-K695R
1.02 0.99 1.05 0.99 1.01 1.02
CldU/IdU
C
30 min
CldU
30 min
IdU
GM00637 (BLM+/+)
KSVS1452 + blm-QVFF-FYF (clone #1)
KSVS1452 + blm-QVFF-FYF (clone #2)
1.11 1.02 1.07
CldU/IdU
D
30 min
CldU
30 min
IdU
GM00637 (BLM+/+)
KSVS1452 (BLMKO)
KSVS1452 + BLM
KSVS1452 + blm-WLVICI
KSVS1452 + blm-K695R
KSVS1452 + blm-WLVICI-K695R
1.01 1.01 1.00 0.97 1.02 1.00
CldU/IdU
E
30 min
CldU
30 min
IdU
GM00637 (BLM+/+)
KSVS1452 (BLMKO)
KSVS1452 + pcDNA3-BLM
KSVS1452 + pcDNA3-blm-K695R
KSVS1452 + pcDNA3-blm-WLVICI
KSVS1452 + pcDNA3-blm-WLVICI-K695R
1.01 1.01 1.00 1.01 0.96 1.00
CldU/IdU

SUPPLEMENTAL INFORMATION

FIGURE LEGENDS

Figure S1. Absence of interaction between BLM and Mcm6 in G2/M. ***(A)*** KSVS1452 (*BLM*^{KO}*)* and GM00637 (*BLM*$^{+/+}$) cells were synchronized at G1/S or blocked at G2/M, and the interaction between endogenous BLM and Mcm6 assessed by co-immunoprecipitation. ***(B)*** Verification by flow cytometry of cell cycle synchronization of KSVS1452 (*BLM*^{KO}*)* and GM00637 (*BLM*$^{+/+}$) cells at G1/S, in S-phase (release from G1/S for 3 hours), or block at G2/M.

Figure S2. Colocalization of BLM, Mcm6 and PML in perturbed and unperturbed S-phase and expression throughout G1 phase. ***(A)*** Confocal images of GM00637 (*BLM*$^{+/+}$) cells showing immunostaining of endogenous BLM and Mcm6 using different antibodies than in Fig. 1E and Fig. 1F (anti-BLM [ab2179, Abcam], anti-Mcm6 [PLA0041, Sigma]). The Mcm6 antibody H-8 (SCBT) was verified by Western blotting ***(B)*** and immunofluorescence microscopy ***(C)***. Three siRNAs from Bioneer (siRNA #4715-1/2/3) and one siRNA from Life Technologies (s8598) targeting human MCM6 expression were used (50 nM) to transfect GM00637 (*BLM*$^{+/+}$) cells using Lipofectamine RNAiMAX (Invitrogen) in Opti-MEM medium. Cells were harvested and Mcm6 levels analyzed 48 hours after transfection. Transfection with scrambled siRNA (Silencer Select Negative Control No. 1, Invitrogen) and immunofluorescence microscopy with only secondary antibody (2^{O}) served as controls. Scr, scrambled siRNA. ***(D)*** Quantification of BLM and Mcm6 foci per nucleus (%) and their colocalization during mid- and late S-phase in GM00637 (*BLM*$^{+/+}$) cells. Foci in 30 nuclei were analyzed; average percentage of foci per nucleus is reported. ***(E)*** Colocalization of BLM and Mcm6 foci with PML foci was quantified in confocal microscopy images of GM00637 (*BLM*$^{+/+}$) cells in the second half of S-phase (5-7 hours after release from G1/S arrest). 30 nuclei were analyzed for each of the indicated time points. Mean ± SD is shown.

Figure S3. Identification of Mcm6 binding sites in the N-terminal tail of BLM. ***(A)*** Disorder scores for all amino acid residues of human BLM were calculated in IUPred (2). A score of >0.5 indicates a discorded residue. ***(B)*** Western blot analysis of expression of BLM and Mcm6 fragments used for two-hybrid analysis of the BLM/Mcm6 interaction. ***(C)*** Two-hybrid analysis of the interaction between the N-terminal domain of Mcm6 (residues 1-325) and fragments of BLM. Mean ± SD from three transfections is shown. Bottom panel shows the Mcm6 and BLM fragments in combination with empty bait and prey vectors. ***(D)*** Two-hybrid analysis of the interaction between fragments of the C-terminal domain of Mcm6 (residues 325-821) and fragments of BLM. Mean ± SD from three transfections is shown. Bottom panel shows the Mcm6 and BLM fragments in combination with empty bait and prey vectors. ***(E)*** Effect of L107A and L108A or F111A mutations in MBD-N of BLM on Mcm6 binding was analyzed by mammalian two-hybrid assay. Mean ± SD from three transfections is shown. ***(F)*** KSVS1452 (*BLM*^{KO}) cells were transfected with plasmids pVP16 expressing the first 120 residues of BLM, or BLM lacking the first 160 residues, the blm-QVF mutant, or empty vector and interaction with endogenous PCNA was assessed by co-immunoprecipitation. BLM peptides and the blm-QVF mutant carry an AD-tag.

Figure S4. Interaction of BLM and BLM mutants with MCM and TopBP1. ***(A)*** Expression levels of BLM mutants transiently expressed from plasmid pVP16 in KSVS1452 (*BLM*^{KO}) cells were assessed by Western blot. ***(B)*** Effect of the milder blm-QVF mutation on BLM/Mcm6 interaction was determined by co-immunoprecipitation of BLM and Western blot for Mcm6. ***(C)*** Effect of deleting the first 160 residues of BLM on interaction with endogenous Mcm6 was assessed by co-immunoprecipitation. KSVS1452 (*BLM*^{KO}) cells were transfected with pVP16 expressing residues 161-1417 of BLM, synchronized at the G1/S boundary, released into S-phase for 3 hours, exposed to 1 μM CPT for 1 hour and nuclear extracts prepared for immunoprecipitation of endogenous Mcm6. ***(D)*** Effect of the blm-VICI mutation in MBD-C on BLM interaction with endogenous Mcm6 was assessed by co-immunoprecipitation. KSVS1452 (*BLM*^{KO}) cells were transfected with pVP16 expressing the blm-VICI mutant, synchronized

at the G1/S boundary, released into S-phase for 3 hours, exposed to 1 μM CPT for 1 hour and nuclear extracts prepared for immunoprecipitation of blm-VICI. ***(E)*** Co-immunoprecipitation of endogenous TopBP1 and the blm-FYF mutant transiently expressed in KSVS1452 (*BLM*^{KO}) cells in unperturbed S-phase and after CPT exposure. ***(F)*** Co-immunoprecipitation of endogenous Mcm6 and TopBP1 with the first 240 residues of BLM, which contain MBD-N and MBD-C but not MBD-D. KSVS1452 (*BLM*^{KO}) cells were transfected with pVP16 expressing the first 240 residues of BLM, synchronized at the G1/S boundary, released into S-phase for 3 hours, exposed to 1 μM CPT for 1 hour and nuclear extracts prepared for immunoprecipitation of endogenous Mcm6 or TopBP1. ***(G)*** Co-immunoprecipitations of endogenous Mcm6 or ***(H)*** endogenous BLM from nuclear extracts of GM00637 (*BLM*$^{+/+}$) and KSVS1452 (*BLM*^{KO}) cells synchronized at G1/S and after release into S-phase for 3 hours. Membranes were probed for endogenous MCM proteins in the order shown, starting with Mcm7 and ending with Mcm5. At the conclusion of the hybridizations, the membrane was again probed with Mcm7 antibody to verify the integrity of protein on the membrane. ***(I)*** Chromatin-bound proteins were extracted from GM00637 (*BLM*$^{+/+}$) cells 6 hours after release from nocodazole block (G1) and 3 hours after release from G1/S block (S) and co-immunoprecipitation of BLM with Mcm6 and other MCM subunits tested. ***(J)*** Whole cell extracts of stable, single-cell clones were analyzed for expression of blm mutants. BLM knockout cell line KSVS1452 and KSVS1452 stably expressing wildtype BLM (KSVS1454) are shown as negative and positive controls, respectively. BLM expression was assessed using BLM antibody A300-110 (Bethyl Laboratories). ***(K)*** Whole cell extracts of stable, single-cell clones were analyzed for expression of the blm-K695R and blm-WLVICI-K695R mutants. Two positive clones for each BLM mutant (Supplemental Table S1) and two negative clones are shown. BLM knockout cell line KSVS1452 and KSVS1452 stably expressing wildtype BLM (KSVS1454) are shown as negative and positive controls, respectively. BLM expression was assessed using BLM antibody A300-110 (Bethyl Laboratories).

Figure S5. Effects of MBD-N, MBD-C, and MBD-D mutations on colocalization of Mcm6 and BLM

in G1, S-phase and after DNA damage. Confocal images of KSVS1452 (*BLM*^{KO}) cells expressing BLM or BLM mutants immunostained for BLM and Mcm6 in ***(A)*** cells in G1 obtained by 6-hour release from nocodazole block ***(B)*** cells in S-phase obtained by 3-hour release from the G1/S boundary, and ***(C)*** cells in mid-S-phase (3 hours) treated with 1 μM CPT for 1 hour and released for 45 minutes into CPT-free media. Anti-BLM C18 (SCBT)] and anti-Mcm6-H8 (SCBT) antibodies were used. ***(D)*** Quantification of BLM or BLM mutant foci for colocalization with Mcm6 in 30 nuclei of cells in G1 phase, unperturbed S-phase and 45 minutes after release from 1-hour CPT exposure. Numbers above columns indicate the percentage of BLM foci that colocalized with Mcm6 foci.

Figure S6. Effect of BLM mutations on DNA replication ***(A)*** Analysis of DNA replication speed in two single-cell clones of the blm-QVFF-FYF mutant by DNA fiber assay. Unperturbed cells were incubated in the presence of CIdU for 30 min and then in the presence of IdU for 30 min, immunostained and imaged on a Keyence fluorescence microscope. A minimum of 100 fibers showing a red region extended by a green region (elongating forks) were analyzed for each cell line. The length of the green region was used to calculate replication speed (kb min^{-1}). Median replication speed is indicated by a black horizontal line. Mann-Whitney test was performed to determine statistical significance of differences to BLM-proficient cell line GM00637: **** $p< 0.0001$. ***(B)*** DNA fiber analysis was used to compare replication speed between *BLM*^{KO} cells (KSVS1452) stably expressing *blm-WLVICI*, *blm-K695R* (clone #13), and a second clone of the stable *blm-WLVICI-K695R* cell line (clone #17). A minimum of 100 fibers were imaged and analyzed as in *(A)*. Median replication speed (kb min^{-1}) is indicated above the scatter dot blot. A Mann-Whitney test was performed to determine statistical significance of differences between the cell lines expressing wildtype BLM or blm mutants: **** $p< 0.0001$; ns, not significant ***(C)*** The WLVICI mutation specifically interrupts the interaction of BLM with Mcm6 in S-phase, but not the interaction of BLM with known BLM binding proteins. Co-immunoprecipitations of BLM or the blm-WLVICI mutant were analyzed for the presence of Mcm6, Topo III, p53 and PCNA. ***(D)*** Co-immunoprecipitation of Cdt1 with Mcm6 in unperturbed GM00637

(*BLM*$^{+/+}$) and KSVS1452 (*BLM*^{KO}) cells and cells exposed to camptothecin. ***(E)*** For analysis of checkpoint activation, whole cell extracts were prepared from exponentially growing, unperturbed KSVS1452 (*BLM*^{KO}) cells stably expressing BLM or blm mutants. As positive controls, replication stress was induced in GM00637 cells (*BLM*$^{+/+}$) by treating with either HU (5 mM for 5 hours) or CPT (1 μM for 24 hours). Cells were lysed in RIPA lysis buffer (supplemented with protease inhibitors and phosphatase inhibitors), cleared by centrifugation at 12 krpm for 15 min, and supernatant analyzed by Western blotting for phosphorylation of RPA and Chk1, using Phospho-RPA (Ser4/Ser8, Bethyl Laboratories) and Phospho-Chk1 (Ser 317, Cell Signaling) antibodies, respectively. ***(F)*** KSVS1452 (*BLM*^{KO}) were transiently transfected with pcDNA3 plasmids expressing K695R, WLVICI, and WLVICI-K695R mutants of BLM. Expression was confirmed by Western blotting of whole cell extracts and probing with BLM antibody A300-110 (Bethyl Laboratories). ***(G)*** DNA fiber analysis was used to compare replication speed between *BLM*^{KO} cells (KSVS1452) transiently transfected with pcDNA3 plasmids expressing BLM or blm mutants. A minimum of 200 DNA fibers were imaged and analyzed as in *(B)*. A Mann-Whitney test was performed to determine statistical significance of differences between the cells expressing the various alleles of BLM (**** $p< 0.0001$).

Figure S7. CldU/IdU ratios of DNA fiber analyses. Ratios were calculated between the length of the first labeling pulse (CldU) and the second labeling pulse (IdU). Unperturbed cells were incubated in the presence of CldU for 30 min and then in the presence of IdU for 30 min, immunostained and imaged on a Keyence fluorescence microscope. A minimum of 100 fibers showing a red region extended by a green region (elongating forks) were analyzed for each cell line. The ratios between the length of the red (CldU) and green region (IdU) were calculated. Median ratios are indicated by a black horizontal line. A median ratio of 1 is indicative of equal DNA replication speed during the two labeling periods. ***(A)*** CldU/IdU ratio for IdU track lengths shown in Figure 5A, ***(B)*** CldU/IdU ratio for IdU track lengths shown in Figure 5B, ***(C)*** CldU/IdU ratio for IdU track lengths shown in Supplemental Figure S6A, ***(D)*** CldU/IdU

ratio for IdU track lengths shown in Supplemental Figure S6B, and ***(E)*** CIdU/IdU ratio for IdU track lengths shown in Supplemental Figure S6G.

REFERENCES

1. Shastri, V.M. and Schmidt, K.H. (2016) Cellular defects caused by hypomorphic variants of the Bloom syndrome helicase gene BLM. *Molecular genetics & genomic medicine*, **4**, 106-119.
2. Dosztanyi, Z., Csizmok, V., Tompa, P. and Simon, I. (2005) The pairwise energy content estimated from amino acid composition discriminates between folded and intrinsically unstructured proteins. *J Mol Biol*, **347**, 827-839.

Table S1. Cell lines constructed for this study

Cell line ID	Parental cell line	Relevant *BLM* genotype	Reference
KSVS1452	GM00637[1]	*BLM* c.del2040_2046/ *BLM* c.delins2036_2041AG	30
KSVS1454	KSVS1452	*BLM*	30
KSVS1455	KSVS1452	*BLM*	30
KSVS1456	KSVS1452	*BLM*	30
KSVS1457	KSVS1452	*blm-QVFF*	This study
KSVS1458	KSVS1452	*blm-QVFF*	This study
KSVS1459	KSVS1452	*blm-QVFF*	This study
KSVS1460	KSVS1452	*blm-FYF*	This study
KSVS1461	KSVS1452	*blm-FYF*	This study
KSVS1462	KSVS1452	*blm-FYF*	This study
KSVS1463	KSVS1452	*blm-WLVICI*	This study
KSVS1464	KSVS1452	*blm-WLVICI*	This study
KSVS1465	KSVS1452	*blm-WLVICI*	This study
KSVS1466	KSVS1452	*blm-QVFF-FYF*	This study
KSVS1467	KSVS1452	*blm-QVFF-FYF*	This study
KSVS1468	KSVS1452	*blm-QVFF-FYF*	This study
KSVS1469	KSVS1452	*blm-QVFF-WLVICI*	This study
KSVS1470	KSVS1452	*blm-QVFF-WLVICI*	This study
KSVS1471	KSVS1452	*blm-QVFF-WLVICI*	This study
KSVES1501	KSVS1452	*blm-K695R* (clone 13)	This study
KSVES1502	KSVS1452	*blm-K695R* (clone 14)	This study
KSVES1503	KSVS1452	*blm-WLVICI-K695R* (clone 11)	This study
KSVES1504	KSVS1452	*blm-WLVICI-K695R* (clone 17)	This study

[1] GM00637 was obtained from the NIGMS Human Genetic Cell Repository at the Coriell Institute.